

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 20:59:14 ; Search time 2144.82 Seconds
(without alignments)

6031.995 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tatatggaagtaagaccctc.....agtagtggggatgcgcc 267

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 .segs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	100.0	267	6	AX105729 Sequence
2	173.4	64.9	269050	1	AL935255 Lactobaci
C 3	173.4	64.9	297050	1	AL935258 Lactobaci
C 4	171.8	64.3	298050	1	AL935260 Lactobaci
C 5	171.8	64.3	298050	1	AL935261 Lactobaci
6	171.8	64.3	324050	1	AL935253 Lactobaci
7	156.4	58.6	317	6	AX105734 Sequence
8	156.4	58.6	317	6	AX105735 Sequence
9	143.6	53.8	326	6	AX105730 Sequence
10	139.4	52.2	335	6	AX105737 Sequence
11	138.2	51.8	326	6	AX105738 Sequence
12	136.4	51.1	336	6	AX105736 Sequence
C 13	131	49.1	177911	1	AE017206 Lactobaci
C 14	131	49.1	183043	6	AX926717 Sequence
15	131	49.1	300478	1	AE017201 Lactobaci
C 16	131	49.1	300886	1	AE017205 Lactobaci
17	131	49.1	349980	6	AX926712 Sequence
18	131	49.1	349980	6	AX926713 Sequence
19	119.2	44.6	338	6	AX105733 Sequence

C 20	115.8	43.4	31702	6	AX413012	AX413012 Sequence
C 21	115.6	43.3	3510	6	CQ788962	CQ788962 Sequence
C 22	115.6	43.3	3510	6	AR218821	AR218821 Sequence
C 23	115.6	43.3	3510	6	BD003733	BD003733 Polynucle
C 24	115.6	43.3	3389	6	BD193765	BD193765 Enterococ
C 25	115.6	43.3	5048	6	BD263589	BD263589 Novel str
26	115.6	43.3	5048	6	AX343071	AX343071 Sequence
27	115.6	43.3	8411	6	CQ788925	CQ788925 Sequence
28	115.6	43.3	8411	6	AR218784	AR218784 Polynucle
29	115.6	43.3	8411	6	BD003696	BD003696 Polynucle
C 30	115.6	43.3	9873	1	AE007481	AE007481 Streptoco
C 31	115.6	43.3	10058	1	AE007489	AE007489 Streptoco
C 32	115.6	43.3	10551	1	AE007319	AE007319 Streptoco
C 33	115.6	43.3	10557	1	AE008537	AE008537 Streptoco
C 34	115.6	43.3	10856	1	AE008546	AE008546 Streptoco
C 35	115.6	43.3	11385	1	AE007495	AE007495 Streptoco
C 36	115.6	43.3	11660	1	AE008386	AE008386 Streptoco
37	115.6	43.3	11915	6	CQ789005	CQ789005 Sequence
38	115.6	43.3	11915	6	AR218864	AR218864 Sequence
39	115.6	43.3	11915	6	BD003776	BD003776 Polynucle
40	115.6	43.3	137952	2	SPNEU1909	AL449931 Streptoco
41	115.6	43.3	232807	2	SPNEU1901	AL449923 Streptoco
42	115.6	43.3	301488	1	AE016950	AE016950 Enterococ
C 43	115.6	43.3	304454	1	AE016956	AE016956 Enterococ
C 44	115.6	43.3	349980	6	AX571765	AX571765 Sequence
45	115.6	43.3	349980	6	AX571766	AX571766 Sequence

ALIGNMENTS

RESULT 1

AX105729

LOCUS

DEFINITION

ACCESSION

VERSION

AX105729 Sequence 1 from Patent WO0123605.
267 bp DNA linear PAT 30-APR-2001
AX105729
AX105729.1 GI:13921742

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 20:53:24 ; Search time 926.081 Seconds

(without alignments)
1706.731 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tatatggaagtaagaccctc.....agtagtgggggatgcgcc 267

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	100.0	267	5	Aaf61566 Lactobaci
2	156.4	58.6	317	5	Aaf61572
3	156.4	58.6	317	5	Aaf61571 L. coryni
4	143.6	53.8	326	5	Aaf61567 Lactobaci
5	139.4	52.2	335	5	Aaf61574 Pediococ
6	138.2	51.8	326	5	Aaf61575 Pediococ
7	136.4	51.1	336	5	Aaf61573 Lactobaci
8	131	49.1	110000	10	Continuation (6 of
9	131	49.1	110000	10	Continuation (8 of
10	131	49.1	110000	10	Continuation (19 o
11	121.6	45.5	110000	9	Adb12064 Alloiococ
12	120	44.9	110000	9	Continuation (6 of
13	120	44.9	110000	9	Continuation (15 o
14	119.2	44.6	338	5	Aaf61570 Lactobaci
15	116.8	43.7	110000	9	Continuation (5 of
16	115.8	43.4	31702	6	Abq67190 Listeria
17	115.6	43.3	3510	2	Aav52186 Streptoco
18	115.6	43.3	3989	2	Aax13296 Enterococ
19	115.6	43.3	3989	6	Abq67194 Listeria
20	115.6	43.3	5048	3	Aaa65735 Streptoco

21	115.6	43.3	5048	6	ABK15101	Abk15101 DNA encod
22	115.6	43.3	8411	2	AAV52149	Aav52149 Streptoco
23	115.6	43.3	11915	2	AAV52229	Aav52229 Streptoco
c 24	115.6	43.3	110000	10	ABS56454_16	Continuation (17 o
c 25	115.6	43.3	110000	10	ABS56454_17	Continuation (18 o
c 26	115.6	43.3	110000	10	ABS56454_18	Continuation (19 o
c 27	115.6	43.3	110000	10	ABS56454_20	Continuation (21 o
c 28	114.2	42.8	1389	6	ABQ70505	Abq70505 Listeria
c 29	114.2	42.8	2631	6	ABQ67189	Abq67189 Listeria
c 30	114.2	42.8	5349	6	ABQ70982	Abq70982 Listeria
c 31	114.2	42.8	110000	6	ABQ67196_0	Continuation (6 of
c 32	114.2	42.8	110000	6	ABQ67196_5	Continuation (3 of
c 33	114.2	42.8	110000	6	ABQ69245_02	Continuation (18 o
c 34	114.2	42.8	110000	6	ABQ69245_17	Continuation (19 o
c 35	114.2	42.8	110000	6	ABQ69245_18	Continuation (20 o
c 36	114.2	42.8	110000	6	ABQ69245_19	Continuation (25 o
c 37	114.2	42.8	110000	6	ABQ69245_24	Continuation (28 o
c 38	114.2	42.8	110000	6	ABQ69245_27	Continuation (2 of
c 39	114.2	42.8	110000	6	ABQ67197_01	Continuation (3 of
c 40	114.2	42.8	110000	6	ABA03041_02	Continuation (25 o
c 41	114.2	42.8	110000	6	ABA03041_24	Continuation (27 o
c 42	114.2	42.8	110000	6	ABA03041_26	Continuation (27 o
c 43	114.2	42.8	319630	6	ABQ67194	Abq67194 Listeria
c 44	114	42.7	9797	2	AAK13487	Aax13487 Enterococ
c 45	114	42.7	9797	6	ABS99282	Abq67194 Listeria

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 23:20:50 ; Search time 5972.62 Seconds
(without alignments)
270.571 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tatatggaagtaagaccct.....agtagtggggatgcgcc 267

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/FCI_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/FCIUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	115.8	43.4	31702	17	US-10-398-221-3
C 2	115.6	43.3	3510	8	US-08-961-527-53
C 3	115.6	43.3	3510	17	US-10-158-844-53
C 4	115.6	43.3	3989	9	US-09-070-927A-359
C 5	115.6	43.3	5048	10	US-09-884-465A-2
C 6	115.6	43.3	8411	8	US-08-961-527-16
C 7	115.6	43.3	8411	17	US-10-158-844-16
C 8	115.6	43.3	11915	8	US-08-961-527-96
C 9	115.6	43.3	11915	17	US-10-158-844-96
C 10	115.6	43.3	2162598	19	US-10-472-928-4979
C 11	115.6	43.3	2162598	19	US-10-472-928-4979

C 12	114.2	42.8	1389	17	US-10-398-221-3318	Sequence 3318, Ap
C 13	114.2	42.8	2631	17	US-10-398-221-2	Sequence 2, Appl
C 14	114.2	42.8	5349	17	US-10-398-221-3795	Sequence 3795, Ap
C 15	114.2	42.8	319630	17	US-10-398-221-7	Sequence 7, Appl
C 16	114.2	42.8	684707	17	US-10-398-221-9	Sequence 9, Appl
C 17	114.2	42.8	684707	17	US-10-398-221-9	Sequence 9, Appl
C 18	114.2	42.8	1163020	17	US-10-398-221-10	Sequence 10, Appl
C 19	114.2	42.8	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
C 20	114.2	42.8	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
C 21	114	42.7	9797	9	US-09-070-927A-550	Sequence 550, App
C 22	114	42.7	22960	9	US-09-070-927A-345	Sequence 345, App
C 23	113.2	42.4	882	17	US-10-398-221-3395	Sequence 3395, Ap
C 24	113.2	42.4	1907	17	US-10-398-221-1847	Sequence 1847, Ap
C 25	113.2	42.4	4199	17	US-10-398-221-3890	Sequence 3890, Ap
C 26	113.2	42.4	6625	17	US-10-398-221-2041	Sequence 2041, Ap
C 27	111.6	41.8	840	8	US-08-781-986A-508	Sequence 508, App
C 28	111.6	41.8	840	17	US-10-329-624-508	Sequence 508, App
C 29	109.6	41.0	400	8	US-08-781-986A-3738	Sequence 3738, Ap
C 30	109.6	41.0	400	17	US-10-329-624-3738	Sequence 3738, Ap
C 31	106	39.7	400	8	US-08-781-986A-3624	Sequence 3624, Ap
C 32	106	39.7	400	17	US-10-329-624-3624	Sequence 3624, Ap
C 33	104.4	39.1	386	8	US-08-781-986A-4064	Sequence 4064, Ap
C 34	104.4	39.1	386	17	US-10-329-624-4064	Sequence 4064, Ap
C 35	101.2	37.9	6591	8	US-08-781-986A-3114	Sequence 3114, Ap
C 36	101.2	37.9	6591	17	US-10-329-624-3114	Sequence 3114, Ap
C 37	100.8	37.8	400	8	US-08-781-986A-3768	Sequence 3768, Ap
C 38	100.8	37.8	400	17	US-10-329-624-3768	Sequence 3768, Ap
C 39	100.6	37.7	400	8	US-08-781-986A-3638	Sequence 3638, Ap
C 40	100.6	37.7	400	17	US-10-329-624-3638	Sequence 3638, Ap
C 41	100.6	37.7	400	17	US-10-329-624-3638	Sequence 3638, Ap
C 42	100.6	37.7	400	17	US-10-329-624-3748	Sequence 3748, Ap
C 43	100.6	37.7	458	8	US-08-781-986A-3757	Sequence 3757, Ap
C 44	100.6	37.7	458	17	US-10-329-624-3757	Sequence 3757, Ap
C 45	100.6	37.7	5134	19	US-10-857-625-162	Sequence 162, App

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:11:20 ; Search time 7983.54 Seconds

(without alignments)
1273.014 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tatatgggaagtaagaccct.....agtagttggggatcgcccc 267

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hlc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163.4	61.2	793	8	BZ369094
2	105.4	39.5	3268	8	BH770998
3	105.4	39.5	6499	8	BH771024
C	58.2	21.8	342	7	CR469421
5	56.4	21.1	690	8	BH687637
C	51.6	19.3	277	7	CR477397
7	50.4	18.9	1258	8	BH770957
8	50.2	18.8	391	8	AQ990586
C	50.2	18.8	607	8	AQ989492
10	49.2	18.4	393	8	CC144308
C	49.2	18.4	453	5	BU003208
C	48.6	18.2	833	9	CL659016
C	48.6	18.2	844	9	CL664279
14	48.6	18.2	872	9	CL662374
C	48.6	18.2	879	9	CL667131
15	47.2	17.7	255	8	BH770635
C	47.2	17.7	333	7	CR470260
18	47	17.6	698	9	AG613316
19	46	17.2	534	9	CL681720
C	46	17.2	664	9	AG613279
C	46	17.2	735	9	CL667389
22	45.8	17.2	544	8	AQ989631
23	45.8	17.2	655	8	AQ990982
C	44.8	16.8	1073	8	AF114216

C	25	44.4	16.6	646	9	CL660916
C	26	44.4	16.6	685	9	CL656043
C	27	44.4	16.6	786	9	CL654528
C	28	44.4	16.6	811	9	CL673498
C	29	44.4	16.6	820	9	CL668273
C	30	44.2	16.6	643	2	AW948147
C	31	44	16.5	381	1	AU180248
C	32	44	16.4	814	7	CNS586292
C	33	43.8	16.4	1101	8	AF029514
C	34	43.6	16.3	351	1	AI903023
C	35	43.2	16.2	1197	8	BZ579062
C	36	43	16.1	343	4	BI895848
C	37	42.6	16.0	330	2	BE092318
C	38	42.6	16.0	694	2	AW948136
C	39	42.6	16.0	730	2	AW948130
C	40	42.6	16.0	738	2	AW948138
C	41	42.4	15.9	158	2	AW858409
C	42	42.4	15.9	282	7	CN025895
C	43	42.4	15.9	518	5	BX548956
C	44	42.4	15.9	548	5	BX548957
C	45	42.4	15.9	791	9	CL670555

ALIGNMENTS

CL660916	PRI0138b
CL656043	PRI0125C
CL654528	PRI0120d
CL673498	PRI019c G
CL668273	PRI0157b
AW948147	RC0-MT001
AU180248	AU180248
CNS586292	USDA-PP_1
AF029514	AF029514
AI903023	QV-BT022
BZ579062	meb2_6160
BI895848	EESTeb01
BE092318	IL2-BT073
AW948136	RC0-MT001
AW948130	RC0-MT001
AW948138	RC0-MT001
AW858409	CN0-CT034
CN025895	UNC-P4clv
BX548956	BX548956
BX548957	BX548957
CL670555	PRI0162b

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 20:59:14 ; Search time 168.694 Seconds
(without alignments)
6031.995 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21
Sequence: 1 ccaagtcacaacgtagttgt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sta.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	21	100.0	21	6	AX105749	Sequence
2	21	100.0	267	6	AX105729	Sequence
3	19.4	92.4	657	5	AY666410	Troglydyt
4	19.4	92.4	665	5	AY666450	Quiscalus
5	19.4	92.4	668	5	AY666444	Quiscalus
6	19.4	92.4	668	5	AY666447	Dendroica
7	19.4	92.4	687	5	AY666190	Geothlypi
8	19.4	92.4	693	5	AY666188	Mniotilta
9	19.4	92.4	693	5	AY666299	Dendroica
10	19.4	92.4	694	5	AY666186	Mniotilta
11	19.4	92.4	694	5	AY666201	Geothlypi
12	19.4	92.4	694	5	AY666258	Fringilla
13	19.4	92.4	694	5	AY666301	Dendroica
14	19.4	92.4	694	5	AY666442	Parula am
15	19.4	92.4	694	5	AY666582	Dendroica
16	19.4	92.4	4692	5	AY327391	Basileute
17	19.4	92.4	4692	5	AY327393	Basileute
18	19.4	92.4	4692	5	AY327395	Basileute
19	19.4	92.4	4692	5	AY327396	Basileute

20	19.4	92.4	4692	5	AY327398	Basileute
21	19.4	92.4	4693	5	AY327394	Basileute
22	19.4	92.4	4693	5	AY327399	Basileute
23	19.4	92.4	4693	5	AY327400	Basileute
24	19.4	92.4	4693	5	AY327401	Basileute
25	19.4	92.4	4694	5	AY327397	Basileute
26	19.4	92.4	4695	5	AY327392	Basileute
27	19.4	92.4	4696	5	AY327389	Dendroica
28	18.4	87.6	666	5	AY666470	Troglydyt
29	18.4	87.6	694	5	AY666367	Molothrus
30	18.4	87.6	694	5	AY666368	Molothrus
c	31	18	2215	3	CVU89789	U89789 Calliphora
32	17.8	84.8	384	5	AY275856	Coeligena
33	17.8	84.8	618	5	AY666465	Dendroica
34	17.8	84.8	656	5	AY666420	Vermivora
35	17.8	84.8	657	5	AY666215	Anthus ru
36	17.8	84.8	659	5	AY666511	Piranga o
37	17.8	84.8	660	5	AY666204	Setophaga
38	17.8	84.8	662	5	AY666455	Dolichony
39	17.8	84.8	663	5	AY666423	Cardinali
40	17.8	84.8	665	5	AY666389	Oenanthe
41	17.8	84.8	666	5	AY666584	Wilsonia
42	17.8	84.8	667	5	AY666516	Sturnella
43	17.8	84.8	668	5	AY666545	Vermivora
44	17.8	84.8	668	5	AY666566	Icterus g
45	17.8	84.8	670	5	AY666453	Dendroica

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 20:53:24 ; Search time 72.8378 Seconds
(without alignments)
1706.731 Million cell updates/sec

Title: us-10-088-666-21

Perfect score: 21

Sequence: 1 ccaagtcaacaacgtagtgt 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	5	Aaf61586 Lactobaci
2	21	100.0	267	5	Aaf61566 Lactobaci
C 3	18	85.7	2215	3	Aaz43884 C. vicina
4	17.8	84.8	207	8	Abx39064 Bovine ES
5	17.8	84.8	211	8	Abx36896 Bovine ES
6	17.8	84.8	229	8	Abx39055 Bovine ES
7	17.8	84.8	239	8	Abx48286 Bovine ES
8	17.8	84.8	242	8	Abx37833 Bovine ES
9	17.8	84.8	247	8	Abx35018 Bovine ES
10	17.8	84.8	292	8	Abx42572 Bovine ES
11	17.8	84.8	301	8	Abx34921 Bovine ES
C 12	17.8	84.8	308	8	Abx45227 Bovine ES
13	17.8	84.8	340	8	Abx37596 Bovine ES
14	17.8	84.8	341	8	Abx37026 Bovine ES
15	17.8	84.8	342	8	Abx46317 Bovine ES
16	17.8	84.8	348	8	Abx44238 Bovine ES
17	17.8	84.8	358	8	Abx43307 Bovine ES
18	17.8	84.8	360	8	Abx36914 Bovine ES
19	17.8	84.8	360	8	Abx47692 Bovine ES
20	17.8	84.8	366	8	Abx43494 Bovine ES

21	17.8	84.8	366	8	Abx48929	Abx48929	Bovine ES
22	17.8	84.8	368	8	Abx39058	Abx39058	Bovine ES
23	17.8	84.8	378	8	Abx37801	Abx37801	Bovine ES
24	17.8	84.8	382	8	Abx35050	Abx35050	Bovine ES
25	17.8	84.8	385	8	Abx45476	Abx45476	Bovine ES
26	17.8	84.8	391	8	Abx45430	Abx45430	Bovine ES
27	17.8	84.8	395	8	Abx37340	Abx37340	Bovine ES
28	17.8	84.8	398	8	Abx41848	Abx41848	Bovine ES
29	17.8	84.8	399	8	Abx44231	Abx44231	Bovine ES
30	17.8	84.8	404	8	Abx35014	Abx35014	Bovine ES
31	17.8	84.8	404	8	Abx37630	Abx37630	Bovine ES
32	17.8	84.8	405	8	Abx42081	Abx42081	Bovine ES
33	17.8	84.8	406	8	Abx47215	Abx47215	Bovine ES
34	17.8	84.8	407	8	Abx44681	Abx44681	Bovine ES
35	17.8	84.8	416	8	Abx46352	Abx46352	Bovine ES
36	17.8	84.8	417	8	Abx44888	Abx44888	Bovine ES
37	17.8	84.8	419	8	Abx42344	Abx42344	Bovine ES
38	17.8	84.8	420	8	Abx40952	Abx40952	Bovine ES
39	17.8	84.8	427	8	Abx42638	Abx42638	Bovine ES
40	17.8	84.8	430	8	Abx40746	Abx40746	Bovine ES
41	17.8	84.8	458	8	Abx43980	Abx43980	Bovine ES
42	17.8	84.8	553	6	Abn73905	Abn73905	Bovine em
43	17.8	84.8	586	6	Abn73190	Abn73190	Bovine em
44	17.8	84.8	606	6	Abn73809	Abn73809	Bovine em
45	17.8	84.8	641	6	Abn73340	Abn73340	Bovine em

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:12:40 ; Search time 21.3153 Seconds

(without alignments)
1612.071 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21

Sequence: 1 ccaagtcacaacgtagtgt 21

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata1/ina/5A COMB.seq:*

2: /cgn2_6/ptodata1/ina/5B COMB.seq:*

3: /cgn2_6/ptodata1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata1/ina/6B COMB.seq:*

5: /cgn2_6/ptodata1/ina/PTUS COMB.seq:*

6: /cgn2_6/ptodata1/ina/backfileseq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.8	80.0	601	4	US-09-949-016-27938
C 2	16.8	80.0	601	4	US-09-949-016-128821
C 3	16.8	80.0	59977	4	US-09-949-016-12259
C 4	16.8	80.0	59978	4	US-09-949-016-15397
C 5	16.4	78.1	422592	4	US-09-949-016-14182
C 6	16.2	77.1	525	4	US-09-248-796A-1527
C 7	16.2	77.1	963	4	US-09-328-352-3811
C 8	16.2	77.1	8878	1	US-08-759-444-2
C 9	16.2	77.1	9880	3	US-08-680-897-1
C 10	15.8	75.2	996	3	US-09-094-557-33
C 11	15.8	75.2	1050	4	US-09-134-000C-2255
C 12	15.8	75.2	1053	3	US-09-071-035-409
C 13	15.8	75.2	2666	4	US-09-524-101D-21
C 14	15.4	73.3	780	4	US-09-248-796A-6461
C 15	15.4	73.3	1380	4	US-09-328-352-537
C 16	15.4	73.3	68778	4	US-09-949-016-16406
C 17	15.2	72.4	601	4	US-09-949-016-39292
C 18	15.2	72.4	601	4	US-09-949-016-76309
C 19	15.2	72.4	735	4	US-09-248-796A-6839
C 20	15.2	72.4	1610	3	US-09-059-769-19
C 21	15.2	72.4	2209	4	US-09-489-847-16
C 22	15.2	72.4	2535	4	US-09-949-016-2216
C 23	15.2	72.4	2565	4	US-09-949-016-1092
C 24	15.2	72.4	3070	4	US-09-799-451-652
C 25	15.2	72.4	4326	4	US-09-949-016-676
C 26	15.2	72.4	5015	4	US-09-949-016-12884
C 27	15.2	72.4	6536	4	US-09-949-016-13958

C 28	15.2	72.4	6538	4	US-09-949-016-12834	Sequence 12834, A
C 29	15.2	72.4	12802	4	US-09-949-016-11792	Sequence 11792, A
C 30	15.2	72.4	13508	4	US-08-956-171E-120	Sequence 120, App
C 31	15.2	72.4	13508	4	US-08-781-986A-120	Sequence 120, App
C 32	15.2	72.4	22374	4	US-09-949-016-14938	Sequence 14938, A
C 33	15.2	72.4	47363	4	US-09-949-016-13420	Sequence 13420, A
C 34	15.2	72.4	142783	4	US-09-949-016-15127	Sequence 15127, A
C 35	15.2	72.4	192956	4	US-09-949-016-14382	Sequence 14382, A
C 36	15.2	72.4	317366	4	US-09-949-016-16001	Sequence 16001, A
C 37	15.2	72.4	393753	4	US-09-949-016-14573	Sequence 14573, A
C 38	15.2	72.4	393753	4	US-09-949-016-14574	Sequence 14574, A
C 39	15.2	72.4	450395	4	US-09-949-016-15473	Sequence 15473, A
C 40	15.2	72.4	818128	4	US-09-949-016-14546	Sequence 14546, A
C 41	15.2	72.4	818128	4	US-09-949-016-14547	Sequence 14547, A
C 42	15.2	72.4	818128	4	US-09-949-016-14548	Sequence 14548, A
C 43	15.2	72.4	818128	4	US-09-949-016-14549	Sequence 14549, A
C 44	15.2	72.4	818128	4	US-09-949-016-14550	Sequence 14550, A
C 45	15.2	72.4	818128	4	US-09-949-016-14551	Sequence 14551, A

ALIGNMENTS

RESULT 1

US-09-949-016-27938/c

; Sequence 27938, Application US/09949016

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 23:20:50 ; Search time 469.757 Seconds
(without alignments)
270.571 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21

Sequence: 1 ccaagtcacaacgtagtgtg 21

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

.Result No.	Score	Query Match	Length	DB ID	Description
1	17.8	84.8	207	9	US-09-960-352-4229 Sequence 4229, Ap
2	17.8	84.8	211	9	US-09-960-352-2061 Sequence 2061, Ap
3	17.8	84.8	229	9	US-09-960-352-4220 Sequence 4220, Ap
4	17.8	84.8	239	9	US-09-960-352-13451 Sequence 13451, A
5	17.8	84.8	242	9	US-09-960-352-2998 Sequence 2998, Ap
6	17.8	84.8	247	9	US-09-960-352-183 Sequence 183, App
7	17.8	84.8	292	9	US-09-960-352-7737 Sequence 7737, Ap
8	17.8	84.8	301	9	US-09-960-352-86 Sequence 86, Appl
c 9	17.8	84.8	308	9	US-09-960-352-10392 Sequence 10392, A
10	17.8	84.8	340	9	US-09-960-352-2761 Sequence 2761, Ap
11	17.8	84.8	341	9	US-09-960-352-2191 Sequence 2191, Ap

12	17.8	84.8	342	9	US-09-960-352-11482 Sequence 11482, A
13	17.8	84.8	348	9	US-09-960-352-9403 Sequence 9403, Ap
14	17.8	84.8	358	9	US-09-960-352-8472 Sequence 8472, Ap
15	17.8	84.8	360	9	US-09-960-352-2079 Sequence 2079, Ap
16	17.8	84.8	360	9	US-09-960-352-12857 Sequence 12857, A
17	17.8	84.8	366	9	US-09-960-352-8659 Sequence 8659, Ap
18	17.8	84.8	366	9	US-09-960-352-14094 Sequence 14094, A
19	17.8	84.8	368	9	US-09-960-352-4223 Sequence 4223, Ap
20	17.8	84.8	378	9	US-09-960-352-2966 Sequence 2966, Ap
21	17.8	84.8	382	9	US-09-960-352-215 Sequence 215, App
22	17.8	84.8	385	9	US-09-960-352-10641 Sequence 10641, A
23	17.8	84.8	391	9	US-09-960-352-10595 Sequence 10595, A
24	17.8	84.8	395	9	US-09-960-352-2505 Sequence 2505, Ap
25	17.8	84.8	398	9	US-09-960-352-7013 Sequence 7013, Ap
26	17.8	84.8	399	9	US-09-960-352-9396 Sequence 9396, Ap
27	17.8	84.8	404	9	US-09-960-352-179 Sequence 179, App
28	17.8	84.8	404	9	US-09-960-352-2795 Sequence 2795, Ap
29	17.8	84.8	405	9	US-09-960-352-7246 Sequence 7246, Ap
30	17.8	84.8	406	9	US-09-960-352-12380 Sequence 12380, A
31	17.8	84.8	407	9	US-09-960-352-9846 Sequence 9846, Ap
32	17.8	84.8	416	9	US-09-960-352-11517 Sequence 11517, A
33	17.8	84.8	417	9	US-09-960-352-10053 Sequence 10053, A
34	17.8	84.8	419	9	US-09-960-352-7509 Sequence 7509, Ap
35	17.8	84.8	420	9	US-09-960-352-6117 Sequence 6117, Ap
36	17.8	84.8	427	9	US-09-960-352-7803 Sequence 7803, Ap
37	17.8	84.8	430	9	US-09-960-352-5911 Sequence 5911, Ap
38	17.8	84.8	458	9	US-09-960-352-9145 Sequence 9145, Ap
39	17.8	84.8	553	11	US-09-876-143-840 Sequence 840, App
40	17.8	84.8	586	11	US-09-876-143-140 Sequence 140, App
41	17.8	84.8	606	11	US-09-876-143-744 Sequence 744, App
42	17.8	84.8	641	11	US-09-876-143-197 Sequence 197, App
43	17.8	84.8	641	11	US-09-876-143-285 Sequence 285, App
44	17.8	84.8	690	11	US-09-876-143-791 Sequence 791, App
45	17.8	84.8	957	11	US-09-876-143-1436 Sequence 1436, Ap

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:11:20 ; Search time 627.919 Seconds
(without alignments)
1273.014 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21
Sequence: 1 ccaagtcacaacgtagttgt 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	85.7	779	8	BH542735
2	17.8	84.8	197	2	BF430206
3	17.8	84.8	204	2	BE477537
4	17.8	84.8	214	2	BE478105
5	17.8	84.8	218	2	BE486429
6	17.8	84.8	261	7	CR383046
7	17.8	84.8	275	7	CO883254
8	17.8	84.8	290	7	CF614527
9	17.8	84.8	313	2	AW426583
10	17.8	84.8	317	5	BQ640947
11	17.8	84.8	369	2	BE483687
12	17.8	84.8	387	2	BE476991
13	17.8	84.8	401	7	CV089879
14	17.8	84.8	413	1	AV613476
15	17.8	84.8	418	7	CF362784
16	17.8	84.8	420	6	CB168898
17	17.8	84.8	421	2	BF230248
18	17.8	84.8	424	2	BE588467
19	17.8	84.8	427	1	AV618453
20	17.8	84.8	432	6	CB166949
21	17.8	84.8	442	2	BE476579
22	17.8	84.8	450	2	BE483083
23	17.8	84.8	451	4	BM432873
24	17.8	84.8	451	5	BP110601

25	17.8	84.8	454	6	CB221784
26	17.8	84.8	471	2	BE487090
27	17.8	84.8	472	2	BE481873
28	17.8	84.8	477	1	AJ691187
29	17.8	84.8	477	2	BE483952
30	17.8	84.8	479	4	BM431900
31	17.8	84.8	493	2	BE483642
32	17.8	84.8	494	4	BM432022
33	17.8	84.8	495	5	BP107620
34	17.8	84.8	498	2	BE481915
35	17.8	84.8	502	2	BE485555
36	17.8	84.8	509	2	BE482287
37	17.8	84.8	512	2	BE481721
38	17.8	84.8	512	2	BE487910
39	17.8	84.8	513	2	BE476202
40	17.8	84.8	513	2	BE480446
41	17.8	84.8	515	1	AV667257
42	17.8	84.8	515	7	CF361479
43	17.8	84.8	519	4	BG690664
44	17.8	84.8	522	2	BE481271
45	17.8	84.8	524	5	BP110809

ALIGNMENTS

CB221784	11L19H7 B
BE487090	175658 BA
BE481873	167477 BA
AJ691187	AJ691187
BE483952	170440 BA
BM431900	1UEJ13H12
BE483642	169866 BA
BM432022	1UEJ15D6
BP107620	BP107620
BE481915	167527 BA
BE485555	172621 BA
BE482287	168021 BA
BE481721	167202 BA
BE487910	177056 BA
BE476202	158828 BA
BE480446	165528 BA
AV667257	AV667257
CF361479	827812 MA
BG690664	339334 BA
BE481271	166655 BA
BP110809	BP110809

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 20:59:14 ; Search time 200.826 Seconds
(without alignments)
6031.995 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25
Sequence: 1 tcgagaataatgaataatatctag 25

Scoring table: IDENTITY NUC

Gapop 10'0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_da.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX105801 Sequence
2	25	100.0	267	6	AX105729 Sequence
C 3	20.4	81.6	1100001	2	AC141815 Apis mell
C 4	20.2	80.8	64701	2	AC079132 Homo sapi
C 5	20.2	80.8	178448	9	AC098805 Homo sapi
C 6	19.8	79.2	153768	2	AC113566 Canis fam
C 7	19.8	79.2	238427	2	AC113234 Canis fam
C 8	19.4	77.6	119113	5	EX005199 Zebrafish
C 9	19.4	77.6	145011	2	CR548634 Danio rer
C 10	19.4	77.6	149163	2	AC071835 Homo sapi
C 11	19.4	77.6	154412	9	HS144F13 Human DNA
C 12	19.4	77.6	195130	9	AL359832 Human DNA
C 13	19.4	77.6	227743	2	CR847529 Danio rer
C 14	19.2	76.8	482	11	CR377191 Arabidops
C 15	19.2	76.8	1074	10	AY425869 Cryptomys
C 16	19.2	76.8	1131	10	AF012235 Cryptomys
C 17	19.2	76.8	35231	5	EX649551 Zebrafish
C 18	19.2	76.8	83537	5	EX004805 Zebrafish
C 19	19.2	76.8	92624	8	AC003000 Arabidops

C	20	19.2	76.8	102029	9	AC133537 Homo sapi
	21	19.2	76.8	123406	8	AC120508 Oryza sat
	22	19.2	76.8	134184	2	AC150028 Canis fam
C	23	19.2	76.8	135129	2	AC148864 Canis fam
	24	19.2	76.8	137923	5	EX640536 Zebrafish
C	25	19.2	76.8	152841	2	AL929463 Danio rer
C	26	19.2	76.8	153438	2	AC117959 Rattus no
	27	19.2	76.8	174846	2	AC141676 Apis mell
	28	19.2	76.8	177722	2	EX928747 Danio rer
C	29	19.2	76.8	189219	9	AC092982 Homo sapi
C	30	19.2	76.8	189355	2	AC053539 Homo sapi
	31	19.2	76.8	194717	9	AC113424 Homo sapi
	32	19.2	76.8	202587	2	AC119862 Mus muscu
C	33	19.2	76.8	202922	2	EX901959 Danio rer
C	34	19.2	76.8	222615	5	AL929345 Zebrafish
	35	19.2	76.8	226614	2	EX957306 Danio rer
C	36	19.2	76.8	268324	5	AL954838 Zebrafish
	37	19.2	76.8	342116	2	AC130918 Rattus no
	38	19.2	76.8	348465	2	AC131165 Rattus no
C	39	19	76.0	164569	2	AC150864 Bos tauru
	40	19	76.0	196455	2	AC151138 Bos tauru
	41	19	76.0	226341	2	AC130020 Rattus no
	42	18.8	75.2	228	6	AX566136 Sequence
	43	18.8	75.2	787	3	AY573636 Drosophil
	44	18.8	75.2	787	3	AY573639 Drosophil
	45	18.8	75.2	788	3	AY573632 Drosophil

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 20:53:24 ; Search time 86.7117 Seconds

(without alignments)
1706.731 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25
Sequence: 1 tggagaataattggaataatatcatg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	5	Aaf61638 Lactobaci
2	25	100.0	267	5	Aaf61566 Lactobaci
3	18.8	75.2	228	8	Abq82965 Human lun
C 4	18.8	75.2	1324	8	Abq82966 Human lun
C 5	18.4	73.6	5064	2	Aav69110 Neisseria
6	18.4	73.6	25426	8	Ada41645 Human sec
7	18.4	73.6	25426	8	Acc50940 Human sec
8	18.4	73.6	25426	10	Add38155 cDNA clon
9	18.4	73.6	25426	10	Ada57777 BAC fragm
10	18.2	72.8	234	10	Adh82432 Enterococ
C 11	18.2	72.8	332	13	Ad51386 Bacterial
C 12	18.2	72.8	468	10	Adh82431 Enterococ
C 13	18.2	72.8	588	12	Ach72871 Human gen
C 14	18.2	72.8	2179	2	Aax13405 Enterococ
C 15	18.2	72.8	2179	6	Ab99200 Enterococ
C 16	18.2	72.8	22620	4	Ab107500 Drosophil
C 17	18.2	72.8	22958	13	Adt05537 Haemophil
18	18.2	72.8	110000	2	Adt05537 Haemophil
C 19	18.2	72.8	163701	13	Abd33351 Murine ca
20	18.2	72.8	349980	13	Adt05648 Haemophil

C 21	18	72.0	1190	2	AAX13651	Aax13651 Enterococ
C 22	18	72.0	1190	6	ABS99446	Ab99446 Enterococ
C 23	18	72.0	5962	6	ABL33286	Ab133286 Human imm
C 24	17.8	71.2	1151	10	ADC08440	Adc08440 Rice DNA
C 25	17.8	71.2	2020	13	ADT05232	Adt05232 Haemophil
C 26	17.8	71.2	3393	8	ABT17845	Abt17845 Aspergill
C 27	17.6	70.4	103	10	ABX83278	Abx83278 Corn ear-
C 28	17.6	70.4	160	6	ABL74381	Ab174381 Corn tass
C 29	17.6	70.4	210	10	ABX83795	Abx83795 Corn ear-
C 30	17.6	70.4	349	6	ABL83657	Ab183657 Human ova
C 31	17.6	70.4	1001	3	AAC57478	Aac57478 Arachidon
C 32	17.6	70.4	1001	3	AAC57477	Aac57477 Arachidon
C 33	17.6	70.4	1486	3	AAC39081	Aac39081 Arabidops
C 34	17.6	70.4	2076	8	ACA33067	Aca33067 Prokaryot
C 35	17.6	70.4	2079	4	AAS52961	Aas52961 Enterococ
C 36	17.6	70.4	2345	4	ABL22259	Ab122259 Drosophil
C 37	17.6	70.4	3212	2	AAV03313	Aav03313 Archaeogl
C 38	17.6	70.4	3212	10	AA156488	Aa156488 Phosphata
C 39	17.6	70.4	5587	4	ABL21402	Ab121402 Drosophil
C 40	17.6	70.4	6032	6	AAS63311	Aas63311 Chemical
C 41	17.6	70.4	8042	4	ABL22258	Ab122258 Drosophil
C 42	17.6	70.4	11429	13	ADS89737	Ad89737 Oligonucl
C 43	17.6	70.4	11429	13	ADS89463	Ad89463 Oligonucl
C 44	17.6	70.4	14429	6	ABL34242	Ab134242 Human imm
C 45	17.6	70.4	14429	6	ABQ67097	Abq67097 Human ang

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:12:40 ; Search time 25.3754 Seconds
(without alignments)
1612.071 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25
Sequence: 1 tcgagaataattgaataatatctag 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B COMB.seq:
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.2	76.8	95566	4	US-09-949-016-11877
2	18.6	75.2	236864	4	US-09-949-016-15753
3	18.6	74.4	211049	4	US-09-949-016-15770
4	18.4	73.6	5064	3	US-08-936-107A-8
5	18.4	73.6	34628	4	US-09-949-016-12304
6	18.4	73.6	34779	4	US-09-949-016-13787
7	18.2	72.8	234	4	US-09-134-000C-317
8	18.2	72.8	468	4	US-09-134-000C-316
9	18.2	72.8	143550	4	US-09-949-016-14143
10	18.2	72.8	1830121	4	US-09-557-884-1
11	18.2	72.8	1830121	4	US-09-643-990A-1
12	17.8	71.2	601	4	US-09-949-016-166500
13	17.8	71.2	30054	4	US-09-949-016-16429
14	17.8	71.2	35322	4	US-09-949-016-11873
15	17.8	71.2	157644	4	US-09-949-016-16179
16	17.8	71.2	157644	4	US-09-949-016-16180
17	17.6	70.4	103	4	US-09-313-294A-1738
18	17.6	70.4	210	4	US-09-313-294A-2255
19	17.6	70.4	1001	3	US-09-641-638-111
20	17.6	70.4	1001	3	US-09-641-638-112
21	17.6	70.4	1001	4	US-10-170-097-111
22	17.6	70.4	1001	4	US-10-170-097-112
23	17.6	70.4	27270	4	US-09-949-016-13822
24	17.4	69.6	25227	4	US-09-949-016-11847
25	17.4	69.6	25227	4	US-09-949-016-14863
26	17.4	69.6	149543	4	US-09-949-016-15947
27	17.4	69.6	1830121	4	US-09-557-884-1
					Sequence 1, Appli

C	28	17.4	69.6	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	29	17.2	68.8	441	4	US-09-710-279-1795	Sequence 1795, Ap
	30	17.2	68.8	462	3	US-09-134-001C-2294	Sequence 2294, Ap
	31	17.2	68.8	467	4	US-09-640-211A-1667	Sequence 1667, Ap
	32	17.2	68.8	473	4	US-09-640-211A-1740	Sequence 1740, Ap
	33	17.2	68.8	533	4	US-09-640-211A-1804	Sequence 1804, Ap
	34	17.2	68.8	563	4	US-09-640-211A-1662	Sequence 1662, Ap
	35	17.2	68.8	601	4	US-09-949-016-186599	Sequence 186599,
	36	17.2	68.8	601	4	US-09-949-016-186600	Sequence 186600,
	37	17.2	68.8	2943	4	US-09-710-279-3983	Sequence 3983, Ap
	38	17.2	68.8	3249	4	US-09-710-279-3622	Sequence 3622, Ap
	39	17.2	68.8	3442	4	US-09-710-279-4030	Sequence 4030, Ap
	40	17.2	68.8	10449	4	US-09-949-016-14475	Sequence 14475, A
	41	17.2	68.8	140725	4	US-09-949-016-17074	Sequence 17074, A
	42	17.2	68.8	363032	4	US-09-949-016-12415	Sequence 12415, A
	43	17.2	68.8	363033	4	US-09-949-016-15754	Sequence 15754, A
	44	17	68.0	601	4	US-09-949-016-63288	Sequence 63288, A
	45	17	68.0	601	4	US-09-949-016-125488	Sequence 125488,

ALIGNMENTS

RESULT 1
US-09-949-016-11877
; Sequence 11877, Application US/09949016

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 23:20:50 ; Search time 559.234 Seconds
(without alignments)
270.571 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25
Sequence: 1 tcgagaataattgaataatctag 25

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	75.2	228	14 US-10-016-349A-108	Sequence 108, App
2	18.8	75.2	1324	14 US-10-016-349A-109	Sequence 109, App
3	18.6	74.4	1206	18 US-10-425-115-119404	Sequence 119404, A
4	18.4	73.6	1891	18 US-10-437-963-45894	Sequence 45894, A
5	18.2	72.8	332	17 US-10-369-493-29816	Sequence 29816, A
6	18.2	72.8	588	16 US-10-029-386-6066	Sequence 6066, Ap
7	18.2	72.8	638	18 US-10-767-701-26220	Sequence 26220, A
8	18.2	72.8	2179	9 US-09-070-927A-468	Sequence 468, App
9	18.2	72.8	163701	18 US-10-322-281-439	Sequence 439, App
10	18.2	72.8	1830121	17 US-10-329-670-1	Sequence 1, Appli
11	18.2	72.8	1830121	18 US-10-158-865-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-016-349A-108

c	12	18	72.0	1190	9	US-09-070-927A-714	Sequence 714, App
c	13	18	72.0	5962	15	US-10-311-455-1259	Sequence 1259, Ap
c	14	17.8	71.2	493	17	US-10-424-599-74009	Sequence 74009, A
c	15	17.8	71.2	1118	13	US-10-027-632-118527	Sequence 118527, A
c	16	17.8	71.2	1118	13	US-10-027-632-118528	Sequence 118528, A
c	17	17.8	71.2	1118	17	US-10-027-632-118527	Sequence 118527, A
c	18	17.8	71.2	1118	17	US-10-027-632-118528	Sequence 118528, A
c	19	17.8	71.2	1710	19	US-10-662-126-26	Sequence 26, Appl
c	20	17.8	71.2	3393	15	US-10-128-714-203	Sequence 203, App
c	21	17.6	70.4	160	9	US-09-294-093B-3755	Sequence 3755, Ap
c	22	17.6	70.4	204	18	US-10-425-115-36493	Sequence 36493, A
c	23	17.6	70.4	332	18	US-10-425-115-104351	Sequence 104351, A
c	24	17.6	70.4	349	9	US-09-867-701-6635	Sequence 6635, Ap
c	25	17.6	70.4	578	17	US-10-425-114-34850	Sequence 34850, A
c	26	17.6	70.4	601	13	US-10-027-632-18543	Sequence 18543, A
c	27	17.6	70.4	601	17	US-10-027-632-18543	Sequence 18543, A
c	28	17.6	70.4	615	13	US-10-027-632-282529	Sequence 282529, A
c	29	17.6	70.4	615	17	US-10-027-632-282529	Sequence 282529, A
c	30	17.6	70.4	771	17	US-10-425-114-1795	Sequence 1795, Ap
c	31	17.6	70.4	998	17	US-10-425-114-19489	Sequence 19489, A
c	32	17.6	70.4	1001	17	US-10-170-097-111	Sequence 111, App
c	33	17.6	70.4	1001	17	US-10-170-097-111	Sequence 112, App
c	34	17.6	70.4	1001	19	US-10-926-684-111	Sequence 111, App
c	35	17.6	70.4	1001	19	US-10-926-684-111	Sequence 112, App
c	36	17.6	70.4	1141	17	US-10-425-114-712	Sequence 712, App
c	37	17.6	70.4	1163	17	US-10-425-114-19232	Sequence 19232, A
c	38	17.6	70.4	1298	17	US-10-425-114-6794	Sequence 6794, Ap
c	39	17.6	70.4	1298	18	US-10-425-115-90866	Sequence 90866, A
c	40	17.6	70.4	1359	17	US-10-424-599-35445	Sequence 35445, A
c	41	17.6	70.4	1370	17	US-10-425-114-1104	Sequence 1104, Ap
c	42	17.6	70.4	1375	17	US-10-425-114-5129	Sequence 5129, Ap
c	43	17.6	70.4	1388	17	US-10-425-114-1028	Sequence 1028, Ap
c	44	17.6	70.4	1388	17	US-10-425-114-3166	Sequence 3166, Ap
c	45	17.6	70.4	1389	17	US-10-425-114-15767	Sequence 15767, A

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:11:20 ; Search time 747.523 Seconds
(without alignments)
1273.014 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25

Sequence: 1 tcgagaataattgaataatatctag 25

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gsa1:*
- 9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20.8	83.2	717	9	AG296763 Mus muscu
C 2	20.2	80.8	460	8	AQ489622 RPCI-11-2
C 3	19.8	79.2	887	9	AL417999 T3 end of
C 4	19.4	77.6	622	9	CL350164 RPCI44_31
5	19.4	77.6	848	8	AZ683885 ENTLP32TF
6	19.4	77.6	877	8	CC141515 NDLP32K2
7	19.4	77.6	898	8	BH133066 ENTPC66TR
8	19.4	77.6	900	8	BH147215 ENTQP41TR
9	19.4	77.6	903	8	BH136872 ENTNA82TR
10	19.2	76.8	214	9	CR398469 Arabidops
11	19.2	76.8	277	9	CG148828 PUFKV46TB
C 12	19.2	76.8	307	9	CL257264 ZMMBB5061
C 13	19.2	76.8	340	6	CD324627 StrPu537
C 14	19.2	76.8	382	9	CE401158 tigr-g88-
C 15	19.2	76.8	386	9	CE624663 tigr-g88-
C 16	19.2	76.8	390	8	BZ632366 PUAHA54TD
C 17	19.2	76.8	405	9	CG148831 PUFKV46TD
18	19.2	76.8	409	8	BZ632406 PUAAT41TB
19	19.2	76.8	413	8	BZ632362 PUAHA54TB
C 20	19.2	76.8	418	8	BZ632408 PUAAT41TD
21	19.2	76.8	424	8	BH170927 SALK_0035
22	19.2	76.8	464	9	CE853568 tigr-g88-
C 23	19.2	76.8	482	7	COS17136 #13DSG29H
C 24	19.2	76.8	568	9	CE345622 tigr-g88-

C 25	19.2	76.8	570	9	CE313026	CE313026 tigr-g88-
C 26	19.2	76.8	583	9	CE029479	CE029479 tigr-g88-
C 27	19.2	76.8	601	9	CE378676	CE378676 tigr-g88-
28	19.2	76.8	630	9	CE407289	CE407289 tigr-g88-
C 29	19.2	76.8	639	9	CE397029	CE397029 tigr-g88-
30	19.2	76.8	641	9	CL379696	CL379696 RPCI44_42
31	19.2	76.8	646	9	CE717195	CE717195 tigr-g88-
C 32	19.2	76.8	685	9	CE745651	CE745651 tigr-g88-
C 33	19.2	76.8	709	9	CL827541	CL827541 OR Cba004
C 34	19.2	76.8	711	9	AG123355	AG123355 Pan trogl
35	19.2	76.8	713	9	CE459772	CE459772 tigr-g88-
36	19.2	76.8	742	9	CE224657	CE224657 tigr-g88-
C 37	19.2	76.8	757	9	CL757754	CL757754 OR Bba012
C 38	19.2	76.8	791	9	CL929820	CL929820 OA Aaa003
C 39	19.2	76.8	833	9	CG048515	CG048515 PUILQ60TB
40	19.2	76.8	911	8	BZ829021	BZ829021 PUGBQ27TD
41	19	76.0	888	9	CG965204	CG965204 MBEMD88TF
C 42	18.8	75.2	402	8	AQ207867	AQ207867 HS_3138_A
43	18.8	75.2	405	1	AI872073	AI872073 t361g11.x
44	18.8	75.2	506	9	CG696733	CG696733 MUGQ_CH25
45	18.8	75.2	574	8	AQ466749	AQ466749 HS_5170_A

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 20:59:14 ; Search time 160.661 Seconds
(without alignments)
6031.995 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20

Sequence: 1 gaggggaagaagtctcttat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX105802 Sequence
2	20	100.0	267	6	AX105729 Sequence
3	18.4	92.0	337	6	CQ455603 Sequence
4	18.4	92.0	6076	10	AF272661 Rattus no
5	18.4	92.0	6109	6	AR564346 Sequence
6	18.4	92.0	6109	6	AX239611 Sequence
7	18.4	92.0	6109	10	AF176645 Mus muscu
8	18.4	92.0	155793	10	AC102821 Mus muscu
9	18.4	92.0	182757	10	AC122484 Mus muscu
10	18	90.0	229813	2	AC117613 Mus muscu
11	17.4	87.0	1907	6	CQ723784 Sequence
12	17.4	87.0	6200	6	AR564347 Sequence
13	17.4	87.0	6200	6	AX239613 Sequence
14	17.4	87.0	6200	9	AF177941 Homo sapi
15	17.4	87.0	6368	6	AX405643 Sequence
16	17.4	87.0	39969	9	HSJ645119 Human DNA
17	17.4	87.0	110000	2	AC109525 Rattus no
18	17.4	87.0	157410	2	AC013816 Homo sapi
19	17.4	87.0	166701	2	AC011457 Homo sapi

20	17.4	87.0	166711	9	AC006116 Homo sapi
21	17.4	87.0	168119	2	AC068686 Homo sapi
22	17.4	87.0	169592	5	BX511100 Zebrafish
23	17.4	87.0	175406	2	AC087128 Mus muscu
24	17.4	87.0	187541	2	AC121560 Mus muscu
25	17.4	87.0	192944	2	AC146902 Callicebu
26	17.4	87.0	194427	9	AC093153 Homo sapi
27	17.4	87.0	207004	5	AL954695 Zebrafish
28	17.4	87.0	207596	2	AC141506 Rattus no
29	17.4	87.0	208657	2	AC046179 Homo sapi
30	17.4	87.0	210636	2	AC105070 Mus muscu
31	17.4	87.0	218244	2	BX571726 Danio rer
32	17.4	87.0	223843	10	AC102595 Mus muscu
33	17.4	87.0	229448	2	AC113690 Rattus no
34	17.4	87.0	229563	10	AC024957 Mus muscu
35	17.4	87.0	235662	2	AC126709 Rattus no
36	17.4	87.0	237019	2	AC094443 Rattus no
37	17.4	87.0	239870	2	AC094970 Rattus no
38	17.4	87.0	243689	2	AC129281 Rattus no
39	17.4	87.0	259178	2	AC108971 Rattus no
40	17.4	87.0	271189	2	AC128515 Rattus no
41	17.4	87.0	304851	2	AC121044 Rattus no
42	17	85.0	101707	2	AC150157 Gallus ga
43	17	85.0	127767	6	CQ868657 Sequence
44	17	85.0	128809	9	AC021648 Homo sapi
45	17	85.0	172825	2	AC020614 Homo sapi

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 20:53:24 ; Search time 69.3694 Seconds

(without alignments)
1706.731 Million cell updates/sec

Title: us-10-088-666-74

Perfect score: 20

Sequence: 1 gagggagaagtctctcttat 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	5	Aaf61639 Lactobaci
2	20	100.0	267	5	Aaf61566 Lactobaci
3	18.4	92.0	337	6	Abn26443 Human ORF
4	18.4	92.0	6109	4	Aah78667 Murine Co
5	17.4	87.0	593	12	Ach68151 Human gen
6	17.4	87.0	6159	12	Adq83504 Human tum
7	17.4	87.0	6200	4	Aah78668 Human COL
8	17.4	87.0	6200	12	Adq19840 Human sof
9	17.4	87.0	6368	6	Abn59647 Novel hum
10	17.4	87.0	6617	12	Adq23958 Human sof
11	17	85.0	127767	13	Abd33584 Murine ca
12	17	85.0	127767	13	Adr67023 Mouse can
13	16.8	84.0	406	9	ACL23170 DNA clone
14	16.8	84.0	514	9	ACL23160 DNA clone
15	16.8	84.0	516	9	ACL23162 DNA clone
16	16.8	84.0	538	9	ACL23156 DNA clone
17	16.8	84.0	548	9	ACL23164 DNA clone
18	16.8	84.0	590	9	ACL23143 DNA clone
19	16.8	84.0	608	9	ACL23167 DNA clone
20	16.8	84.0	617	9	ACL23169 DNA clone

C 21	16.8	84.0	623	9	ACL23148	ACL23148 DNA clone
C 22	16.8	84.0	631	9	ACL23157	ACL23157 DNA clone
C 23	16.8	84.0	637	9	ACL23168	ACL23168 DNA clone
C 24	16.8	84.0	655	9	ACL23158	ACL23158 DNA clone
C 25	16.8	84.0	679	9	ACL23163	ACL23163 DNA clone
C 26	16.8	84.0	681	9	ACL23145	ACL23145 DNA clone
C 27	16.8	84.0	692	9	ACL23161	ACL23161 DNA clone
C 28	16.8	84.0	717	9	ACL23159	ACL23159 DNA clone
C 29	16.8	84.0	722	9	ACL23171	ACL23171 DNA clone
C 30	16.8	84.0	110000	2	AAK91990_04	Continuation (5 of
C 31	16.8	84.0	110000	4	AAK95240_11	Continuation (12 o
C 32	16.8	84.0	110000	4	AAK96733_11	Continuation (12 o
C 33	16.8	84.0	110000	6	ABT00010_11	Continuation (12 o
C 34	16.8	84.0	110000	6	ABT01503_11	Continuation (12 o
C 35	16.8	84.0	110000	12	ADH77486_11	Continuation (12 o
C 36	16.8	84.0	175561	8	AAD55694	Ad55694 Human THB
C 37	16.8	84.0	175561	12	ADL08129	Adl08129 Human Gen
C 38	16.8	84.0	273254	3	AAK81914	AAK81914 Chlamydia
C 39	16.4	82.0	255	6	ABK81965	Abk81965 Human dys
C 40	16.4	82.0	465	6	ABK75767	Abk75767 Bacillus
C 41	16.4	82.0	702	5	AAK92053	AAK92053 DNA encod
C 42	16.4	82.0	1340	6	AAK37239	AAK37239 Human dys
C 43	16.4	82.0	1477	12	ADN60337	Adn60337 B. lichen
C 44	16.4	82.0	1667	6	AAK37235	AAK37235 Human dys
C 45	16.4	82.0	1991	6	AAK37231	AAK37231 Human dys

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:12:40 ; Search time 20.3003 Seconds
(without alignments)
1612.071 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20

Sequence: 1 gagggagaagtctcttat 20

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.4	92.0	6109	4	US-09-795-061-1
2	17.4	87.0	6200	4	US-09-795-061-3
3	16.8	84.0	46319	4	US-09-949-016-12526
4	16.8	84.0	46323	4	US-09-949-016-13267
5	16.8	84.0	1230025	4	US-09-198-452A-1
6	16.8	84.0	1230230	4	US-09-438-185A-1
7	16.4	82.0	5952	4	US-09-687-875A-1
8	16.4	82.0	13977	3	US-09-484-970B-60
9	15.8	79.0	239	3	US-09-443-184-18
10	15.8	79.0	244	3	US-09-443-184-19
11	15.8	79.0	267	3	US-09-443-184-17
12	15.8	79.0	601	4	US-09-949-016-41020
13	15.8	79.0	601	4	US-09-949-016-41021
14	15.8	79.0	601	4	US-09-949-016-44921
15	15.8	79.0	601	4	US-09-949-016-44922
16	15.8	79.0	601	4	US-09-949-016-130621
17	15.8	79.0	601	4	US-09-949-016-130622
18	15.8	79.0	601	4	US-09-949-016-130623
19	15.8	79.0	601	4	US-09-949-016-130624
20	15.8	79.0	601	4	US-09-949-016-145008
21	15.8	79.0	601	4	US-09-949-016-145009
22	15.8	79.0	601	4	US-09-949-016-145010
23	15.8	79.0	601	4	US-09-949-016-157254
24	15.8	79.0	601	4	US-09-949-016-157255
25	15.8	79.0	601	4	US-09-949-016-157256
26	15.8	79.0	601	4	US-09-949-016-157276
27	15.8	79.0	601	4	US-09-949-016-157277

C 28	15.8	79.0	601	4	US-09-949-016-157278	Sequence 157278, A
C 29	15.8	79.0	601	4	US-09-949-016-157298	Sequence 157298, A
C 30	15.8	79.0	601	4	US-09-949-016-157299	Sequence 157299, A
C 31	15.8	79.0	601	4	US-09-949-016-157300	Sequence 157300, A
C 32	15.8	79.0	3001	4	US-09-539-333D-156	Sequence 156, Appl
C 33	15.8	79.0	3182	1	US-07-797-556-5	Sequence 5, Appl
C 34	15.8	79.0	3182	1	US-07-943-843-1	Sequence 1, Appl
C 35	15.8	79.0	3182	1	US-08-347-003-1	Sequence 1, Appl
C 36	15.8	79.0	3591	1	US-07-943-843-5	Sequence 5, Appl
C 37	15.8	79.0	3591	1	US-08-347-003-5	Sequence 5, Appl
C 38	15.8	79.0	5245	4	US-09-949-016-4210	Sequence 4210, Ap
C 39	15.8	79.0	5252	4	US-09-949-016-338	Sequence 338, App
C 40	15.8	79.0	7953	4	US-09-949-016-16886	Sequence 16886, A
C 41	15.8	79.0	25992	4	US-09-949-016-17308	Sequence 17308, A
C 42	15.8	79.0	26000	4	US-09-843-376-10	Sequence 10, Appl
C 43	15.8	79.0	27632	4	US-09-949-016-12903	Sequence 12903, A
C 44	15.8	79.0	36456	4	US-09-949-016-12404	Sequence 12404, A
C 45	15.8	79.0	36457	4	US-09-949-016-13031	Sequence 13031, A

ALIGNMENTS

RESULT 1

US-09-795-061-1

; Sequence 1, Application US/09795061

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 23:20:50 ; Search time 447.387 Seconds
(without alignments)
270.571 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20

Sequence: 1 gagggagaagtctcttat 20

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	6109	10 US-09-795-061-1	Sequence 1, Appli
2	18	90.0	465	18 US-10-425-115-45008	Sequence 45008, A
3	17.4	87.0	593	16 US-10-029-386-1346	Sequence 1346, Ap
4	17.4	87.0	6200	10 US-09-795-061-3	Sequence 3, Appli
5	17.4	87.0	6200	18 US-10-723-860-2659	Sequence 2659, Ap
6	17.4	87.0	6617	18 US-10-723-860-2659	Sequence 6778, Ap
7	17	85.0	127767	18 US-10-322-281-797	Sequence 797, Appl
8	16.8	84.0	175561	14 US-10-017-721-3	Sequence 3, Appli
9	16.8	84.0	175561	17 US-10-235-192A-48	Sequence 48, Appli
10	16.8	84.0	1230025	17 US-10-289-762-1	Sequence 1, Appli
11	16.8	84.0	1503841	9 US-09-795-668-1	Sequence 1, Appli

100	16.8	84.0	1503841	9 US-09-795-668-1	Sequence 1, Appli
101	16.8	84.0	1503841	9 US-09-946-807-1	Sequence 1, Appli
102	16.4	82.0	25	19 US-10-719-900-626239	Sequence 626239, A
103	16.4	82.0	201	18 US-10-719-993-24492	Sequence 24492, A
104	16.4	82.0	255	17 US-10-149-736-7	Sequence 7, Appli
105	16.4	82.0	255	19 US-10-964-536-7	Sequence 7, Appli
106	16.4	82.0	465	9 US-09-974-300-3058	Sequence 3058, Ap
107	16.4	82.0	688	13 US-10-027-632-102170	Sequence 102170, A
108	16.4	82.0	688	13 US-10-027-632-102171	Sequence 102171, A
109	16.4	82.0	688	17 US-10-027-632-102170	Sequence 102170, A
110	16.4	82.0	688	17 US-10-027-632-102171	Sequence 102171, A
111	16.4	82.0	1340	10 US-09-845-416-11	Sequence 11, Appli
112	16.4	82.0	1667	10 US-09-845-416-7	Sequence 7, Appli
113	16.4	82.0	1991	10 US-09-845-416-3	Sequence 3, Appli
114	16.4	82.0	2022	18 US-10-437-963-57769	Sequence 57769, A
115	16.4	82.0	3446	10 US-09-845-416-14	Sequence 14, Appli
116	16.4	82.0	3510	10 US-09-845-416-12	Sequence 12, Appli
117	16.4	82.0	3531	10 US-09-845-416-10	Sequence 10, Appli
118	16.4	82.0	3858	10 US-09-845-416-9	Sequence 9, Appli
119	16.4	82.0	3999	10 US-09-845-416-6	Sequence 6, Appli
120	16.4	82.0	414	10 US-09-845-416-2	Sequence 2, Appli
121	16.4	82.0	414	10 US-09-845-416-32	Sequence 32, Appli
122	16.4	82.0	4476	10 US-09-845-416-31	Sequence 31, Appli
123	16.4	82.0	4498	10 US-09-845-416-30	Sequence 30, Appli
124	16.4	82.0	4825	10 US-09-845-416-29	Sequence 29, Appli
125	16.4	82.0	4848	10 US-09-845-416-35	Sequence 35, Appli
126	16.4	82.0	4966	10 US-09-845-416-28	Sequence 28, Appli
127	16.4	82.0	4990	10 US-09-845-416-34	Sequence 34, Appli
128	16.4	82.0	5060	10 US-09-845-416-36	Sequence 36, Appli
129	16.4	82.0	5149	10 US-09-845-416-27	Sequence 27, Appli
130	16.4	82.0	5339	17 US-10-149-736-40	Sequence 40, Appli
131	16.4	82.0	5339	19 US-10-964-536-40	Sequence 40, Appli
132	16.4	82.0	5417	17 US-10-149-736-39	Sequence 39, Appli
133	16.4	82.0	5417	19 US-10-964-536-39	Sequence 39, Appli

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:11:20 ; Search time 598.018 Seconds

(without alignments)
1273.014 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20
Sequence: 1 gagggagaagttctcttat 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gse1:
9: gb_gse2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	95.0	613	4	BI508715
2	18.4	92.0	419	6	CB764501
3	18.4	92.0	445	6	CB744432
4	18.4	92.0	467	6	CB714203
C 5	18.4	92.0	536	8	BH047608
6	18.4	92.0	650	4	BI113486
7	18.4	92.0	662	5	BQ829603
C 8	18.4	92.0	665	6	BY742218
C 9	18.4	92.0	696	2	BE113195
10	18.4	92.0	748	4	BG921699
11	18.4	92.0	796	7	CO397391
12	18.4	92.0	881	2	BF123606
C 13	18.4	92.0	1015	3	AK020873
C 14	17.4	87.0	205	4	BF998912
C 15	17.4	87.0	348	4	BG955594
C 16	17.4	87.0	374	9	CG639825
17	17.4	87.0	425	1	AA317772
18	17.4	87.0	429	5	BY455173
19	17.4	87.0	454	5	BQ832471
20	17.4	87.0	468	1	AL046182
21	17.4	87.0	590	4	BM704665
22	17.4	87.0	595	6	CB177816
23	17.4	87.0	658	7	CN305165
24	17.4	87.0	671	5	BX918106

25	17.4	87.0	736	9	AG165391
26	17.4	87.0	740	6	CB517692
C 27	17.4	87.0	753	9	CL283567
28	17.4	87.0	843	9	CL865206
29	17.4	87.0	958	2	BF344853
30	17.4	87.0	1026	8	BZ248710
C 31	17	85.0	268	2	BB434970
C 32	17	85.0	296	4	BI296803
C 33	17	85.0	584	1	AU016700
34	17	85.0	1025	9	CL452767
35	16.8	84.0	203	4	BM440965
36	16.8	84.0	240	1	AJ482932
37	16.8	84.0	240	1	AJ482934
C 38	16.8	84.0	262	8	AQ471789
39	16.8	84.0	273	5	BX558902
40	16.8	84.0	282	5	BU970698
41	16.8	84.0	293	6	CB078133
42	16.8	84.0	300	1	AJ482936
43	16.8	84.0	300	1	AJ482937
44	16.8	84.0	334	4	BM497325
45	16.8	84.0	360	1	AJ460905

ALIGNMENTS

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OM nucleic --nucleic search, using sw model

Run on: April 4, 2005, 14:37:50 ; Search time 0.001 Seconds
(without alignments)
240.300 Million cell updates/sec

Title: us-10-088-666-1
Perfect score: 267
Sequence: 1 tatatggaagtaagaccct.....agtagtggggatcgcccc 267

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 25 seqs, 450 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 25 summaries

Database : lissdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match %	Length DB ID	Description
1	20	7.5	20	1 US-08-944-974A-1 Sequence 1, Appli
2	17.4	6.5	20	1 US-09-198-452A-3383 Sequence 3383, Ap
C 3	15.8	5.9	21	1 US-09-422-978-9420 Sequence 9420, Ap
C 4	15	5.6	15	1 US-08-461-210-30 Sequence 30, Appl
C 5	14.2	5.3	20	1 US-09-073-567-15 Sequence 15, Appl
C 6	14.2	5.3	20	1 US-09-073-567-37 Sequence 37, Appl
7	14.2	5.3	20	1 US-09-198-452A-4575 Sequence 4575, Ap
C 8	13.4	5.0	15	1 US-08-461-210-29 Sequence 29, Appl
C 9	13.4	5.0	15	1 US-08-461-210-31 Sequence 31, Appl
10	13.2	4.9	18	1 US-08-450-905B-135 Sequence 135, App
C 11	13.2	4.9	18	1 US-09-213-768-33 Sequence 33, Appl
12	13.2	4.9	18	1 US-09-161-244-53 Sequence 53, Appl
13	13.2	4.9	18	1 US-07-982-759F-135 Sequence 135, App
14	13.2	4.9	18	1 US-08-584-040-6219 Sequence 6219, Ap
C 15	13.2	4.9	18	1 US-09-371-772B-2981 Sequence 2981, Ap
16	13.2	4.9	18	1 US-09-544-398B-584 Sequence 584, App
C 17	13.2	4.9	18	1 US-09-543-771B-584 Sequence 584, App
18	13.2	4.9	18	1 US-09-685-664B-2981 Sequence 2981, Ap
C 19	13	4.9	16	1 US-09-479-005A-399 Sequence 399, App
C 20	13	4.9	16	1 US-09-479-005A-400 Sequence 400, App
21	12.8	4.8	18	1 US-08-373-124A-15 Sequence 15, Appl
22	12.8	4.8	18	1 US-08-808-303-13 Sequence 13, Appl
23	12.8	4.8	18	1 US-08-435-628-15 Sequence 15, Appl
24	12.8	4.8	18	1 US-09-344-579-10 Sequence 10, Appl
25	12.8	4.8	18	1 US-08-996-533-13 Sequence 13, Appl

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:39:10 ; Search time 0.001 Seconds
(without alignments)
85.440 Million cell updates/sec

Title: us-10-088-666-1
Perfect score: 267
Sequence: 1 tatatggaagtaagaccct.....agtagtgggggagtcgcc 267

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 0.5

Searched: 7 seqs, 160 residues

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 7 summaries

Database : 1pubdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.2	7.2	25	1 US-10-719-900-325614	Sequence 325614,
2	17.6	6.6	25	1 US-10-719-900-325615	Sequence 325615,
3	17.6	6.6	25	1 US-10-719-900-781674	Sequence 781674,
4	17.4	6.5	20	1 US-10-289-762-3383	Sequence 3383, Ap
5	16.2	6.1	22	1 US-10-315-317-24	Sequence 24, Appl
6	16.2	6.1	22	1 US-10-315-217-24	Sequence 24, Appl
7	15.8	5.9	21	1 US-10-349-143-9420	Sequence 9420, Ap

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:42:29 ; Search time 0.001 Seconds

(without alignments)
831.438 Million cell updates/sec

Title: us-10-088-666-1

Perfect score: 267

Sequence: 1 tatatggaagtaagaccctc.....agtagtggggatgcgcc 267

Scoring table: IDENTITY NUC

Gapop 10₀ , Gapext 0.5

Searched: 59 seqs, 1557 residues

Total number of hits satisfying chosen parameters: 118

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 59 summaries

Database : 1rngdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	100.0	267	1	AAF61566
2	26.6	10.0	33	1	AAF61566
3	25.8	9.7	30	1	AAH50148
4	25.8	9.7	30	1	AAH50137
5	25.8	9.7	31	1	AAH50158
6	25.6	9.6	32	1	AAF61672
7	25.4	9.5	27	1	AAH50194
8	25	9.4	25	1	AAH50194
9	25	9.4	25	1	AAH50194
10	25	9.4	25	1	AAH50194
11	25	9.4	25	1	AAH50194
12	23.4	8.8	26	1	AAF61668
13	23	8.6	23	1	AAF61618
14	23	8.6	32	1	AAF61670
15	22.8	8.5	31	1	AAH50147
16	21.4	8.0	23	1	AAF61619
17	21.4	8.0	23	1	AAF61616
18	21.4	8.0	23	1	AAF61614
19	21	7.9	21	1	AAF61586
20	21	7.9	21	1	AAF61684
21	21	7.9	23	1	AAF61613
22	20.4	7.6	22	1	ABA90523
23	20	7.5	20	1	AAQ37096
24	20	7.5	20	1	AAQ67115
25	20	7.5	20	1	AAQ67115
26	20	7.5	20	1	AAQ67115
27	20	7.5	20	1	AAQ67115
28	19.8	7.4	23	1	AAF61615
29	19.8	7.4	23	1	AAF61617
30	19.4	7.3	21	1	AAF61666
31	19	7.1	27	1	AAH50193
32	18.8	7.0	22	1	ADC21238
33	18.8	7.0	22	1	ADL22828

C	34	18	6.7	18	1	AAF61628	Unidentified 23S r
	35	17.8	6.7	21	1	AAF61665	Lactobacillus sp 2
	36	17.4	6.5	20	1	AAH94057	PCR primer used to
	37	16.8	6.3	20	1	ADO85452	TagMan PCR primer
	38	16.4	6.1	18	1	AAF61626	Unidentified 23S r
	39	16.4	6.1	18	1	AAF61636	Unidentified 23S r
	40	16.4	6.1	18	1	AAF61632	Unidentified 23S r
	41	16.4	6.1	18	1	AAF61637	Unidentified 23S r
	42	16.4	6.1	22	1	AAH01916	blatEM resistance
	43	16.2	6.1	22	1	ADO42863	Primer of the inve
	44	15.8	5.9	21	1	AAH75064	Human biallelic ma
	45	15.6	5.8	22	1	AAH75064	Linker for constru
	46	15.2	5.7	18	1	AAF61625	Unidentified 23S r
	47	15.2	5.7	20	1	ABS52237	Plant vector PCR p
	48	15.2	5.7	21	1	AAZ26236	Human polymorphic
	49	15	5.6	15	1	ABK97321	#810 5Srev PCR pri
	50	15	5.6	20	1	ABL44318	Human chromosome 1
	51	14.8	5.5	18	1	AAF61635	Unidentified 23S r
	52	14.8	5.5	18	1	AAF61631	Unidentified 23S r
	53	14.8	5.5	18	1	AAF61630	Unidentified 23S r
	54	14.8	5.5	18	1	AAF61629	Unidentified 23S r
	55	14.8	5.5	18	1	AAF61634	Unidentified 23S r
	56	14.8	5.5	19	1	AAH92954	Antisense oligonuc
	57	14.8	5.5	20	1	ADK75919	Chimeric phosphoro
	58	14.8	5.5	20	1	ADK75951	Chimeric phosphoro
	59	14.8	5.5	20	1	ADK75223	Chimeric phosphoro

ALIGNMENTS

RESULT 1
AAF61566
ID AAF61566 standard; DNA; 267 BP.
XX

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:44:14 ; Search time 0.001 Seconds
(without alignments)
24.402 Million cell updates/sec

Title: us-10-088-666-21

Perfect score: 21

Sequence: 1 ccaagtcacacagtagtggt 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 0.5

Searched: 54 seqs, 581 residues

Total number of hits satisfying chosen parameters: 108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 60 summaries

Database : 211ssdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13.2	62.9	18	1	US-08-450-905B-135
2	13.2	62.9	18	1	US-07-982-759F-135
C 3	11.8	56.2	15	1	US-08-389-564B-28
C 4	11.8	56.2	15	1	US-08-466-047B-28
C 5	11.2	53.3	16	1	US-08-303-004-5
C 6	9.4	44.8	11	1	US-09-798-542-15
7	8.8	41.9	15	1	US-08-389-564B-28
8	8.8	41.9	15	1	US-08-466-047B-28
C 9	8.4	40.0	10	1	US-08-222-177A-407
10	8.4	40.0	10	1	US-08-206-176-11
C 11	8.4	40.0	10	1	US-08-206-176-11
12	8.4	40.0	10	1	US-08-756-506-10
C 13	8.4	40.0	10	1	US-08-756-506-10
14	8.4	40.0	10	1	US-09-042-071-28
C 15	8.4	40.0	10	1	US-09-042-071-28
16	8.4	40.0	11	1	US-09-249-155A-37
17	8.4	40.0	11	1	US-09-249-155A-266
18	8.4	40.0	12	1	US-09-427-834A-18
C 19	8	38.1	10	1	US-09-632-538C-7
C 20	8	38.1	10	1	US-09-627-536-7
C 21	8	38.1	10	1	US-09-641-540-7
22	8	38.1	11	1	US-08-327-516-8
23	8	38.1	11	1	US-09-281-766-8
24	8	38.1	11	1	US-09-612-858-8
25	8	38.1	11	1	US-09-957-995A-8
26	7.8	37.1	11	1	US-09-798-542-15
27	7.4	35.2	10	1	US-09-263-790-35
28	7.4	35.2	10	1	US-09-721-777-17
C 29	7.4	35.2	10	1	US-08-171-718-49
C 30	7.4	35.2	10	1	US-08-478-087-49
C 31	7.4	35.2	10	1	US-08-522-384-7
C 32	7.4	35.2	10	1	US-08-522-384-19
33	7.4	35.2	10	1	US-08-522-384-82

C 34	7.4	35.2	10	1	US-08-927-165A-33	Sequence 33, Appl
C 35	7.4	35.2	10	1	US-09-425-799-14	Sequence 14, Appl
36	7.4	35.2	10	1	US-09-336-946B-18	Sequence 18, Appl
37	7.4	35.2	10	1	US-09-508-753B-145	Sequence 145, Appl
38	7.4	35.2	10	1	US-09-508-753B-221	Sequence 221, Appl
C 39	7.4	35.2	10	1	US-09-508-753B-249	Sequence 249, Appl
40	7.4	35.2	10	1	US-08-894-454-154	Sequence 154, Appl
C 41	7	33.3	10	1	US-08-586-875-2	Sequence 2, Appl
42	7	33.3	10	1	US-08-631-751A-13	Sequence 13, Appl
43	7	33.3	10	1	US-08-828-010-4	Sequence 4, Appl
C 44	7	33.3	10	1	US-08-522-384-8	Sequence 8, Appl
C 45	7	33.3	10	1	US-08-522-384-23	Sequence 23, Appl
C 46	7	33.3	10	1	US-08-988-384-2	Sequence 2, Appl
47	7	33.3	10	1	US-08-991-789A-88	Sequence 88, Appl
48	7	33.3	10	1	US-09-062-451-88	Sequence 88, Appl
49	7	33.3	10	1	US-09-598-326-88	Sequence 88, Appl
50	7	33.3	10	1	US-09-154-750A-25	Sequence 25, Appl
C 51	7	33.3	10	1	US-09-914-259-125	Sequence 125, Appl
52	7	33.3	10	1	US-09-508-753B-376	Sequence 376, Appl
C 53	7	33.3	10	1	US-09-508-753B-436	Sequence 436, Appl
C 54	7	33.3	10	1	US-10-003-830-2	Sequence 2, Appl
55	7	33.3	10	1	US-09-289-198-88	Sequence 88, Appl
56	7	33.3	10	1	US-09-429-755-88	Sequence 88, Appl
57	7	33.3	10	1	US-09-822-250A-13	Sequence 13, Appl
58	7	33.3	10	1	US-10-034-350A-13	Sequence 13, Appl
59	7	33.3	10	1	US-09-699-295-88	Sequence 88, Appl
C 60	7	33.3	10	1	5244792-18	Patent No. 5244792